

Sequence Listing.txt
SEQUENCE LISTING

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<110>  LUKYANOV, SERGEY A
        SHAGIN, DMITRY A
        YANUSHEVICH, YURY G

<120>  FLUORESCENT PROTEINS AND CHROMOPROTEINS FROM NON-AEQUOREA
        HYDROZOA SPECIES AND METHODS FOR USING SAME

<130>  U 015745-9
<140>  10/532,681
<141>  2005-04-26

<160>  23

<170>  PatentIn version 3.4

<210>  1
<211>  784
<212>  DNA
<213>  Phialidium sp.

<400>  1
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ggttatggag atgcaagtgt tggtaaagt ttgatccaat tcattctgcac aactggagat    180
gtaccagttc catggtcaac ttagtaaca acacttactt atggtgcaca atgcttcgcc    240
aaatatggtc cagaattaaa ggattttctac aagagttgca tgcctgaagg ctatgtgcag    300
gagcgtacaa tcacatttga aggggacgga gtatttaaaa ctgcgcgtga agttacattt    360
gaaaacggat ctgtttataa ccgagtcataa cttaattggac aaggatttaa gaaagacgga    420
catgtgcttg gaaagaatct tgaattcaat ttcacacctc attgtcttta catttgggga    480
gatcaggcta atcatgtgtt gaagtctgct ttcataaatta tgcattgagat tactggatca    540
aaagaagact tcattgttgc agaccacacc caaatgaaca caccatttgg tgggtggacca    600
gtccatgttc ctgaatacca tcataataca taccatgtca ctctcagcaa agatgttact    660
gatcacaggg ataacatgag ctgtgttgaa accgtacggg ctgtggattg cagaaaaaca    720
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ttat                                             784

<210>  2
<211>  234
<212>  PRT
<213>  Phialidium sp.

<400>  2
Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1          5          10          15

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Sequence Listing.txt

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Glu Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Ile Thr Tyr His Val Thr Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 3

<211> 705

<212> DNA

<213> Artificial sequence

<220>

<223> phiYFP-Y1 mutant of the phiYFP

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<400> 3
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aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttgcccaaat atggtccaga attaaaggat 240
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gacggagtat ttaaaactcg cgctgaagtt acatttga aaacggatctgt ttataaccga 360
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ttcaatttca cacctcattg tctttacatt tggggagatc aggctaataca tggtttgaag 480
tctgctttca aaattatgca tgagattact ggatcaaaaag gagacttcat tgtgcagac 540
cacaccacaa tgaacacacc cattggtggt ggaccagtcc atgtccctga ataccatcat 600
atgacatacc atgtcactct cagcaaaagat gttactgac acagggataa catgagcttg 660
gttgaaacgc tacgggctgt ggattgcaga aaaacatac tttaa 705

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<210> 4
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-Y1 mutant of the phiYFP

<400> 4

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Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1      5      10      15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20      25      30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35      40      45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50      55      60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65      70      75      80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
85      90      95

Thr Phe Glu Gly Asp Gly Val Phe Lys Thr Arg Ala Glu Val Thr Phe
100     105     110

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Sequence Listing.txt

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Met His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Thr Tyr His Val Thr Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Val Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 5
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-M0 mutant of the phiYFP

<400> 5
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aaagtgtgat cccaattcat ctgcacaact ggagatgtac cagtcccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttgcaccaat atggtccaga attaaaggat 240
ttctacaaga gttgcatgcc tgaaggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggaaact ttaaaactcg cgtgaagtt acatttgaaa acggatctgt ttataaccga 360
gtcaaaactta atggacaagg atttaagaaa gacggacatg tgcttggaag gaatttgaa 420
ttcaatttca cacttcattg tctttacatt tggggagatc aggtcaatca tggtttgaag 480
tctgctttca aaattcgcca tgagattact ggatcaaaag gagacttcat tgttgacagc 540
cacacccaaa tgaacacacc cattggtggt ggaccagtc atgtccctga aaaccatcat 600

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atgagctacc atgtcaagct cagcaaagat gttactgac acagggataa catgagcttg 660
 aaggaacccg tacgggctgt ggattgcaga aaaacatatac tttaa 705

<210> 6
 <211> 234
 <212> PRT
 <213> Artificial sequence

<220>
 <223> phiYFP-M0 mutant of the phiYFP

<400> 6

Met Pro Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
 1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
 20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Arg His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Sequence Listing.txt

Val His Val Pro Glu Asn His His Met Ser Tyr His Val Lys Leu Ser
195 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 7
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-M1 mutant of the phiYFP

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aatgttgatg gacacacatt ctccattaga ggtaaagggt atggagatgc aagtgttggt 120
aaagttgatg cccaattcat ctgcacaact ggagatgtac cagttccatg gtcaacttta 180
gtaacaacac ttacttatgg tgcacaatgc ttgcaccaat atggtccaga attaaaggat 240
ttctacaaga gttgcattgcc tgatggctat gtgcaggagc gtacaatcac atttgaaggg 300
gacggaaact ttaaaactcg cgctgaagtt acatttgaaa acggatctgt ttataaccga 360
gtcaacttta atggacaagg atttaagaaa gacggacatg tgcttggaaa gaatcttgaa 420
ttcaatttca cacotcattg totttacatt tggggagatc aggcataatca tggtttgaag 480
tgtgctttca aaattttgcca tgagattact ggatcaaaaag gagacttcat tgttgagagc 540
cacacccaaa tgaacacacc cattgggtgtt ggaccagtc atgtccctga ataccatcat 600
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<210> 8
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M1 mutant of the phiYFP

<400> 8

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Sequence Listing.txt

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
 35 40 45

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
 50 55 60

Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
 65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
 85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
 100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
 115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 9
 <211> 705
 <212> DNA
 <213> Artificial sequence

<220>
 <223> humanized version of the phiYFP-M1

<400> 9
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aaggtggatg ccaggttcac ctgcaccacc ggcgatgtgc ccgtgccctg gagcacctg 180
gtgaccaccc tgacctacgg cgcaccagtc ttccccaagt acggcccca gctgaaggat 240
ttctacaaga gctgcattgcc cgatggctac gtgcaggagc gcaccatcac cttcgagggc 300
gatggcaatt tcaagaccgg cgcggagggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggg cttcaagaag gatggccacg tgctgggcaa gaatctggag 420
ttcaatttca ccccccaactg cctgtacatc tggggcgatc aggccaatca cggcctgaag 480
agcgccttca agatctgccca cgagatcacc ggcagcaagg gcgatttcac cgtggccgat 540
cacaccaga tgaatacccc catcggcggc ggccccgtgc acgtgcccca gtaccaccac 600
atgagctacc acgtgaagct gagcaaggat gtgaccgatc accgcgataa tatgagcctg 660
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<210> 10
<211> 234
<212> PRT
<213> Artificial sequence

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<220>
<223> humanized version of the phiYFP-M1

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<400> 10

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Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

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```

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

```

```

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

```

```

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

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Thr Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

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Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

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Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

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Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe

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Sequence Listing.txt

115

120

125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
 130 135 140

Pro His Cys Leu Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
 145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
 165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Pro
 180 185 190

Val His Val Pro Glu Tyr His His Met Ser Tyr His Val Lys Leu Ser
 195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
 210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
 225 230

<210> 11
 <211> 1047
 <212> DNA
 <213> Anthomedusae species

<220>
 <221> misc_feature
 <223> hydromedusa 1 from sub-order Anthomedusae

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 ggtgtcaaaa atttacgttc tagaaaattgc agtacggaag aaaaaccogt catacttggt 180
 gcaatgacag aaacatttca gaaaaaattg ccatataagt tagaattgga tggagatggt 240
 gatgggcaaa catttaaggt tattggtgag ggcgttgggg atgcaaccac tgggtgaatt 300
 gaaggaataa atgtttgtac agaaggagaa gtccctattt catgggttcc gctcatcacc 360
 tcattaagtt atggtgcgaa atgttttggt cgatatccaa atgaaataaa tgattttttc 420
 aaaagtactt ttcttctgg atactatcaa gaaagaaaaa ttacatatga gaatgatggt 480
 gtttagaaaa cagcagctaa aattactatg gaaagtgggt caatagtga tagaataaat 540
 gtgaaaggca caggcttcga taaagatggt catgtatgcc aaaaaaatct tgaatcctcc 600
 cctccttcga caacatatgt tgttcccag ggagaaggta ttcgaatcat ctatagaaac 660

Sequence Listing.txt

atctatccaa caaaagatgg tcactatggt gttgccgaca cacagcaagt aaatcgacca	720
attagagcac aaggaacatc agctatccca acatatcatc acattaaatc gaaagttgat	780
ctttcaacag atccagaaga aaataaagat catattatca tcaaagaaac caactgcgca	840
tttgacgtg atttttctta agatttccga tttgcatcaa gattgaaaaa ctaaataaag	900
ataggtaaaa aaaatatgtc tttgatgtta catacagtat tgatataagc ttcaaagaaa	960
tatattttca aataaaacttt ataaaattag gaattcttga atatataaac taaacotttt	1020
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<210> 12
 <211> 262
 <212> PRT
 <213> Anthomedusae species
 <220>
 <221> misc_feature
 <223> hydromedusa 1 from sub-order Anthomedusae
 <400> 12

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Gly	Val	Lys	Asn	Leu	Arg	Ser	Arg	Asn	Cys	Ser	Thr	Glu	Glu	Lys	Pro
		20						25					30		

Val	Ile	Leu	Gly	Ala	Met	Thr	Glu	Thr	Phe	Gln	Lys	Lys	Leu	Pro	Tyr
	35					40						45			

Lys	Leu	Glu	Leu	Asp	Gly	Asp	Val	Asp	Gly	Gln	Thr	Phe	Lys	Val	Ile
	50				55					60					

Gly	Glu	Gly	Val	Gly	Asp	Ala	Thr	Thr	Gly	Val	Ile	Glu	Gly	Lys	Tyr
65				70					75					80	

Val	Cys	Thr	Glu	Gly	Glu	Val	Pro	Ile	Ser	Trp	Val	Ser	Leu	Ile	Thr
		85						90					95		

Ser	Leu	Ser	Tyr	Gly	Ala	Lys	Cys	Phe	Val	Arg	Tyr	Pro	Asn	Glu	Ile
		100						105					110		

Asn	Asp	Phe	Phe	Lys	Ser	Thr	Phe	Pro	Ser	Gly	Tyr	His	Gln	Glu	Arg
	115						120					125			

Lys	Ile	Thr	Tyr	Glu	Asn	Asp	Gly	Val	Leu	Glu	Thr	Ala	Ala	Lys	Ile
	130					135					140				

Thr	Met	Glu	Ser	Gly	Ala	Ile	Val	Asn	Arg	Ile	Asn	Val	Lys	Gly	Thr

Sequence Listing.txt

cgagagcaat caagattcct ggacctcatt tcgttactgt gataatcaaa cagatgaaag 720
 atacaagcga caagcgtgat catgtgtgtc aacgtgaagt cacctacgct cactcagttc 780
 cacgcatcac ttctgctatc taaacatcat tcttaaaagg ggaacatgca catcatactt 840
 cagtgtgagg gtcagtggtga gggctctttag atgtcaattt gtcgcagggtg tcacacggcg 900
 tcgtttagat gttgaaggac gaaatgcgac aaagagatta atagagactc atatttttat 960
 gtagaatcga ttcattcagc ccattggtaa cctttttggt attttatcat cttattattg 1020
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<210> 14
 <211> 232
 <212> PRT
 <213> Anthomedusae species
 <220>
 <221> misc_feature
 <223> hydromedusa 2 from sub-order Anthomedusae
 <400> 14

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 20 25 30
 Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
 35 40 45
 Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
 50 55 60
 Gln Tyr Gly Glu Pro Phe Phe Ala Lys Tyr Pro Asn Gly Ile Ser His
 65 70 75 80
 Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Thr Ile Asp Arg Thr Val
 85 90 95
 Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
 100 105 110
 Asp Gly Thr Cys Val Ile Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
 115 120 125
 Gln Pro Asp Gly Pro Ile Met Lys Asp Gln Leu Val Asp Ile Leu Pro
 130 135 140

Sequence Listing.txt

Thr Glu Thr His Met Phe Pro His Gly Ser Asn Ala Val Arg Gln Leu
145 150 155 160

Cys Tyr Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175

Phe Asp Ser Lys Leu Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190

Gly Pro His Phe Val Thr Val Ile Ile Lys Gln Met Lys Asp Thr Ser
195 200 205

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 15

<211> 699

<212> DNA

<213> Artificial sequence

<220>

<223> S3-2 mutant of the hm2CP from a hydromedusa 2 from sub-order
Anthomedusae

<400> 15
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gacttcaacg tacatgctgt gtgcgaaacc gggaaatcc caatgtcatg gaaaccatt 180
tgtcacctta tccaatacgg ggagccattc tttgcaagat atcccaacgg catcagccat 240
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gacggcacta tgacgtctca ccacacctat gagttggacg gcacctgtgt cgtttccagg 360
ataacggtta attgtcagcg atttcaacct gatggaccaa tcatgagaga ccagcttggt 420
gatatacctgc caaacgagac acatatgttc cctcatggac ccaatgctgt cagacaattg 480
gctttcatag gcttcacgac agctgatggt ggtctcatga tgtcacattt tgattcgaaa 540
atgacattca atgggtcgag agcaatcaag attcctggac ctcatctcgt cactaccata 600
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tacgtcact cagttccag catcacttct gctatctaa 699

<210> 16

<211> 232

<212> PRT

Sequence Listing.txt

<213> Artificial sequence

<220>

<223> S3-2 mutant of the hm2CP from a hydromedusa 2 from sub-order Anthomedusae

<400> 16

Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
1 5 10 15Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
20 25 30Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
35 40 45Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
50 55 60Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
65 70 75 80Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
85 90 95Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
100 105 110Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
115 120 125Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
130 135 140Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
145 150 155 160Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
165 170 175Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
180 185 190Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
195 200 205Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Sequence Listing.txt

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 17
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the
phiYFP-M1

<400> 17
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aagggtgatg ccagttcat ctgcaccacc ggcatgtgc cgtgccctg gagcacctg 180
gtgaccaccc tgcctacagg cgcctcagtc ttgcctcagt acggccccga gctgaaggat 240
ttctacaaga gctgcatgcc cgatgggtac gtgcaggagc gcaccatcac ctctgagggc 300
gatggcaatt tcaagaccgc cgcgaggtg accttcgaga atggcagcgt gtacaatcgc 360
gtgaagctga atggccaggc ctcaagaag gatggccacg tgcggggcaa gaatctggag 420
ttcaatttca cccccactg ccagtacatc tggggcgatc aggcacatca cggcctgaag 480
agcgccctta agatctgcca cgagatcacc ggcagcaagg gcgatttcat cgtggccgat 540
cacaccacga tgaatacccc catcgggcgc ggccccgtgc acgtgccga gtaccaccac 600
atgagcacc acgtgaagct gagcaaggat gtgaccgac accgcgataa tatgagcgtg 660
aaggagaccg tgcgcgccgt ggattgccga acagcctacc tgtga 705

<210> 18
<211> 234
<212> PRT
<213> Artificial sequence

<220>
<223> phiYFP-M1G1 mutant, derived from humanized version of the
phiYFP-M1

<400> 18

Met Ser Ser Gly Ala Leu Leu Phe His Gly Lys Ile Pro Tyr Val Val
1 5 10 15

Glu Met Glu Gly Asn Val Asp Gly His Thr Phe Ser Ile Arg Gly Lys
20 25 30

Gly Tyr Gly Asp Ala Ser Val Gly Lys Val Asp Ala Gln Phe Ile Cys
35 40 45

Sequence Listing.txt

Thr Thr Gly Asp Val Pro Val Pro Trp Ser Thr Leu Val Thr Thr Leu
50 55 60

Ser Tyr Gly Ala Gln Cys Phe Ala Lys Tyr Gly Pro Glu Leu Lys Asp
65 70 75 80

Phe Tyr Lys Ser Cys Met Pro Asp Gly Tyr Val Gln Glu Arg Thr Ile
85 90 95

Thr Phe Glu Gly Asp Gly Asn Phe Lys Thr Arg Ala Glu Val Thr Phe
100 105 110

Glu Asn Gly Ser Val Tyr Asn Arg Val Lys Leu Asn Gly Gln Gly Phe
115 120 125

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Cys Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Val
210 215 220

Arg Ala Val Asp Cys Arg Thr Ala Tyr Leu
225 230

<210> 19
<211> 705
<212> DNA
<213> Artificial sequence

<220>
<223> phiYFP-M1C1 mutant, derived from humanized version of the
phiYFP-M1

<400> 19
atgtccagcg gcgcccagct gttccacggc aagatcccct acgtggtgga gatggagggc 60
aatgtggatg gccacacctt cagcatccgc ggcaagggtc acggcgatgc cagcgtgggc 120
aagggtgatg ccagttcat ctgcaccacc ggcgatgtgc ccgtgccctg gagcaccctg 180

Sequence Listing.txt

gtgaccaccc	tgtcctgggg	cgccacgtgc	ttcgccaagt	acggccccga	gctgaaggat	240
ttctacaaga	gctgcatgcc	cgatggctac	gtgcaggagc	gcaccatcac	cttcgagggc	300
gatggcaatt	tcaagaccgc	cgccgaggtg	accttcgaga	atggcagcgt	gtacaatcgc	360
gtgaagctga	aaggccaggg	cttcaagaag	gatggccacg	tgctgggcaa	gaatctggag	420
ttcaatttca	ccccccacta	ccagtacatc	tgggcgcatc	aggccaatca	cggcctgaag	480
agcgccttca	agatctgcca	cgagatcacc	ggcagtaagg	gcgatttcat	cgtggccgat	540
cacaccacga	tgaatacccc	catcgggcgc	ggccccgtgc	acgtgccoga	gtaccaccac	600
atgagcacc	acgtgaagct	gagcaaggat	gtgaccgac	accgcgataa	tatgagcctg	660
aaggagacct	tcgcgcgcgt	ggattgccgc	aagacctacc	tgtga		705

<210> 20
 <211> 234
 <212> PRT
 <213> Artificial sequence

<220>
 <223> phiYFP-M1C1 mutant, derived from humanized version of the
 phiYFP-M1

<400> 20

Met	Ser	Ser	Gly	Ala	Gln	Leu	Phe	His	Gly	Lys	Ile	Pro	Tyr	Val	Val
1			5						10					15	

Glu	Met	Glu	Gly	Asn	Val	Asp	Gly	His	Thr	Phe	Ser	Ile	Arg	Gly	Lys
			20					25					30		

Gly	Tyr	Gly	Asp	Ala	Ser	Val	Gly	Lys	Val	Asp	Ala	Gln	Phe	Ile	Cys
		35					40					45			

Thr	Thr	Gly	Asp	Val	Pro	Val	Pro	Trp	Ser	Thr	Leu	Val	Thr	Thr	Leu
		50				55					60				

Ser	Trp	Gly	Ala	Gln	Cys	Phe	Ala	Lys	Tyr	Gly	Pro	Glu	Leu	Lys	Asp
65					70					75				80	

Phe	Tyr	Lys	Ser	Cys	Met	Pro	Asp	Gly	Tyr	Val	Gln	Glu	Arg	Thr	Ile
			85						90					95	

Thr	Phe	Glu	Gly	Asp	Gly	Asn	Phe	Lys	Thr	Arg	Ala	Glu	Val	Thr	Phe
			100					105					110		

Glu	Asn	Gly	Ser	Val	Tyr	Asn	Arg	Val	Lys	Leu	Lys	Gly	Gln	Gly	Phe
		115					120					125			

Sequence Listing.txt

Lys Lys Asp Gly His Val Leu Gly Lys Asn Leu Glu Phe Asn Phe Thr
130 135 140

Pro His Tyr Gln Tyr Ile Trp Gly Asp Gln Ala Asn His Gly Leu Lys
145 150 155 160

Ser Ala Phe Lys Ile Cys His Glu Ile Thr Gly Ser Lys Gly Asp Phe
165 170 175

Ile Val Ala Asp His Thr Gln Met Asn Thr Pro Ile Gly Gly Gly Pro
180 185 190

Val His Val Pro Glu Tyr His His Met Ser Thr His Val Lys Leu Ser
195 200 205

Lys Asp Val Thr Asp His Arg Asp Asn Met Ser Leu Lys Glu Thr Leu
210 215 220

Arg Ala Val Asp Cys Arg Lys Thr Tyr Leu
225 230

<210> 21

<211> 699

<212> DNA

<213> Artificial sequence

<220>

<223> humanized version of the S3-2 mutant of hm2CP from a hydromedusa
2 from sub-order Anthomedusae

<400> 21

atggaggcg	gccccgcct	gttccagagc	gacatgacct	tcaaaatctt	catcgacggc	60
gtggtgaacg	gccagaagt	caccatcgtg	gccgacggca	gcagcaagtt	ccccacggc	120
gacttcaacg	tgcaecgct	gtcgcgagacc	ggcaagctgc	ccatgagctg	gaagcccatc	180
tgccacctga	tccagtacgg	cgagcccttc	ttgcccgcct	accccaacgg	catcagccac	240
ttcgcccagg	agtgettccc	cgaggggcctg	agcatcgacc	gcaccgtgcg	cttcgagaac	300
gacggcacca	tgaccagcca	ccacacctac	gagctggacg	gcacctcgct	ggtgagccgc	360
atcacctgta	actgcgacgg	cttcagcccc	gacggccccca	tcattgcgga	ccagctgggtg	420
gacatcctgc	ccaacgagac	ccacatgttc	ccccacggcc	ccaacgcctg	gcgccagctg	480
gccttcacg	gcttcaccac	cgccgacggc	ggcctgatga	tgagccactt	cgacagcaag	540
atgaccttca	acgggacggc	cgccatcaag	atccccggcc	cccacttcgt	gaccaccatc	600
accaagcaga	tgaaggacac	cagcgacaag	cgcgaccacg	tgtgccagcg	cgaggtgacc	660
tacgcccaca	gcgtgccccg	catcaccacg	gccatctga			699

Sequence Listing.txt

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<210> 22
<211> 232
<212> PRT
<213> Artificial sequence

<220>
<223> humanized S3-2 mutant of hm2CP from a hydromedusa 2 from
      sub-order Anthomedusae

<400> 22
Met Glu Gly Gly Pro Ala Leu Phe Gln Ser Asp Met Thr Phe Lys Ile
 1              5              10              15

Phe Ile Asp Gly Val Val Asn Gly Gln Lys Phe Thr Ile Val Ala Asp
      20              25              30

Gly Ser Ser Lys Phe Pro His Gly Asp Phe Asn Val His Ala Val Cys
      35              40              45

Glu Thr Gly Lys Leu Pro Met Ser Trp Lys Pro Ile Cys His Leu Ile
      50              55              60

Gln Tyr Gly Glu Pro Phe Phe Ala Arg Tyr Pro Asn Gly Ile Ser His
 65              70              75              80

Phe Ala Gln Glu Cys Phe Pro Glu Gly Leu Ser Ile Asp Arg Thr Val
      85              90              95

Arg Phe Glu Asn Asp Gly Thr Met Thr Ser His His Thr Tyr Glu Leu
      100             105             110

Asp Gly Thr Cys Val Val Ser Arg Ile Thr Val Asn Cys Asp Gly Phe
      115             120             125

Gln Pro Asp Gly Pro Ile Met Arg Asp Gln Leu Val Asp Ile Leu Pro
      130             135             140

Asn Glu Thr His Met Phe Pro His Gly Pro Asn Ala Val Arg Gln Leu
 145             150             155             160

Ala Phe Ile Gly Phe Thr Thr Ala Asp Gly Gly Leu Met Met Ser His
      165             170             175

Phe Asp Ser Lys Met Thr Phe Asn Gly Ser Arg Ala Ile Lys Ile Pro
      180             185             190

Gly Pro His Phe Val Thr Thr Ile Thr Lys Gln Met Lys Asp Thr Ser
      195             200             205

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Sequence Listing.txt

Asp Lys Arg Asp His Val Cys Gln Arg Glu Val Thr Tyr Ala His Ser
210 215 220

Val Pro Arg Ile Thr Ser Ala Ile
225 230

<210> 23
<211> 238
<212> PRT
<213> Aequorea victoria

<400> 23

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
180 185 190

Sequence Listing.txt

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235